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PR   21-JUL-1997;   97US-0053329.
PR   04-AUG-1997;   97US-0054642.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Bowtell D, Killian A;
XX
PI
PA
XX
WPI; 1999-106060/09.
DR   P-PSDB; AAY00627.
XX
PT   New isolated vertebrate telomerase genes - used to develop products
PT   for treating cancers or for organ regeneration, nerve cell or brain
PT   cell growth following injury or bone marrow transplantation
XX
PS   Claim 3; Fig 1; 134PP; English.
XX
CC   This sequence encodes the human telomerase of the invention. Primers that
CC   amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem
CC   could be administered in the bone marrow transplant context). As well,
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury.
XX
SQ   Sequence 3964 BP; 661 A; 1337 C; 1257 G; 709 T; 0 other;
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alignment_scores:

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     Quality:  5866.00
     Ratio:    5.247
Percent Similarity:  98.763        Length:   1132
                                   Gaps:     1
                     Percent Identity:  98.763
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alignment_block:
US-09-502-424-46:

Align seg 1/1 to: AAX18254

Align seg 1/1 to: AAX18254   from: 1 to: 3964

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1251 TGCGGTCACCCAGCAGCCGGTGCTGTGTGCCGGGGAGAAGCCCAGGGCT 1300

434 erValAlaAlaProGluGlyGluAspThrAspProArgGlyGluValGln
1301 CTGTGGGCGGCGGCCCCGAGGAGGAGGACACAGACCCCGTCGGGTGCAG 1350

451 LeuLeuArgGlnHisSerSerProTrpGlnValTyrGlyPheValArgAl
1351 CTGCTCCCCCAGCACAGCAGCCCCTGGCAGGTGTACGGCCTTCGTGCGGGC 1400

467 aCysLeuArgArgLeuValProGlyProGlyLeuTrpGlySerArgHisAsnG
1401 CTGCCTCGCCGCCTGGTGCCCGGCCCCGGCCTCTGGGGCTCCAGGCACAACG 1450

484 luArgArgPheLeuArgAsnThrLysLysProPheLeuSerLeuGlyLysHis
1451 AACGCCGCCTTCCTCAGGAACACAAAGAAGTTCATCTCCCTGGGAAGCAT 1500

501 AlaLysLeuSerLeuGlnGluThrTrpLysMetSerValArgAspCy
1501 GCCAAGCTCTCGCTGCAGGAGACGTGGAAGATGAGCGTGGGGCTG 1550

517 sAlaThrProLeuArgArgSerProGlyValGlyCysValProAlaAlaGluH
1551 CGCTTGGGCTCGGACAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGC 1600

534 isArgLeuArgGluGluLeuIleLeuAlaLysPheLeuHisTrpLeuMetSer
1601 ACCGGTCTGCGTGAGGAGGAGATCCTGGCCAAGTTCCTGCACTGGCTGATGAGT 1650

551 ValTyrValValGluLeuLeuArgSerPheProGluTyrValThrGluThrTh
1651 GTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTATGTCCACGGAGACCAC 1700

567 rPheGlnLysLysAsnArgLeuPhePheTyrArgGlySerValTrpSerLysL
1701 GTTTCAAAAGAACAGGCTCTTTTTTCTACCGGAAGAGTGTCTGGAGCAAGT 1750

584 euGlnSerIleGlyIleLeuArgGlnHisHisLeuArgValGlnLeuArgGlu
1751 TGCAAAGCATTGGGAATCACAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG 1800

601 LeuSerGlyIleValLeuArgGlnHisArgGluAlaAlaArgProAlaLeuLe
1801 CTGTCGGGAAGCAGAGGTCAGGCACCATCGGGAAGCACCGGGCCGCCCGCT 1850

617 uThrSerArgLeuArgPheIleProLysProAspGlyLeuArgProIleV
1851 GACGTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTG 1900

634 aIAsnMetAspTyrValValGlyAlaAargThrArgArgGlnLysLysArg
1901 TGAACATGGACTACGTCGTGGGAGCCAAGACGTTCCGCAGAGAAAAGAGG 1950

651 AlaGluLeuThrSerArgValLysAlaLeuPheSerValLeuAsnTy
1951 GCCGAGCGGTCTCACCTCGAGGTGAAGGCACTGTTCAGCGTGCTCAACTA 2000

667 rGluArgGlnArgArgProGlyLeuLeuGlyLeuAlaSerValLeuGlyLeuA
2001 CGAGCGGCAGCGGCGGCCCGGCCTCCTGGGCCTGGCCTCTGTGCTGGGCCTGG 2050

684 spAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln
2051 ACGATATCCACAGGGCCTGGCGGCCACCTTCGTGCTGCGTGTGCGGGCCCAG 2100

701 AspProProGlyLeuThrTyrPheValLys
2101 GACCCGCCGGGCCTGACGTACTTTGTCAAGGTGGAGTGGACGGGCCGTA 2150

711 .........
2151 CGACACCAATCCCCAGGACAGCAGGCTCACGGAGGTCATCGGCAGCATCATCA 2200
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722 ysProGlnAsnThrTyrCysValArgArgThrTyrAlaValValGlnLysAla
2201 AACCCCAGAACACGTACTGCGGTCGGAGGACTTATGCCGTGGTCCAGAAGGCC 2250

739 AlaHisGlyHisValArgLysTyrAlaPheLeuSerHisValSerThrLeuTh
2251 GCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTGTCTTACCTTGAC 2300

755 rAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuSerGlnGluThrS
2301 AGACCTCCAGCCGTACATGCGACAGTTCGTGGCCCACCTGTCCCAGGAGACCA 2350

772 erProLeuArgAspAlaValValAlaIleGluGluSerSerLeuAsnGlu
2351 GCCCGCTGAGGGATGCCGTCGTCGCCATCGAGGAGAGCTCTCTGAATGAG 2400

789 AlaSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisSerAl
2401 GCCAGCAGGTGGCCCTTCTGCGACGTGTTCCTTCAGTGCCACCACGC 2450

805 aValAargIleGluArgGlyLysSerTyrValValGlnIleCysGlnProGlnGln
2451 CGTGCGCANTCAGGGGCAAGTCCTTACGTCCAGTGCCAGGGGGATCCGGCAGG 2500

822 lySerIleLeuSerThrLeuLeuCysSerTyrGlyTyrGlyAspMetGlu
2501 GCTCCATCCTTCCAGCGGCTGCTCTGCAGCTATGGCTACGGGCACATGGAG 2550

839 AsnLysSerLeuPheAlaGlyIleLeuArgArgAspGlyLeuLeuLeuArgLeuVa
2551 AACAAGTCGTTTGCCGGGATCCTGCGGCGGGACGGCCTCCTGCTCCGGCTTGGT 2600

855 lAspAspPheLeuValAlaThrProHisLeuThrHisSerThrPheLeu
2601 GGATGATTTCTTGTTGGTGGCCACCCCTCACCTCAGGCGGTTTGGT 2650

872 euArgThrArgLeuArgGlyValProGluTyrGlyCysSerValValAsnLeu
2651 TCAGGACCCGTGGTCCGGAGGTCCCTGAGTATGGCTGCTCGGTGAACTTG 2700

889 ArgLysThrValValAlaAsnPheProValGluAspGluLeuGlyLeuGlyTh
2701 CGGAAGACAGTGGTGGCAAACTTCCCTGTAGAAGACGAGCTGGGTGGCCAC 2750

905 rAlaPheValGlnMetProAlaHisGlyLeuLeuPheProTrpCysGlyLeuL
2751 GGCTTTGTGCAGATGCCGGCCCACGGGCTTATTCCCCTGGTGCGGCCTGC 2800

922 euLeuAspThrArgThrLeuGlnSerAspTyrSerSerTyrAla
2801 TGCTGGATACCCGGACCCTGCAGAGCGACTACTCCAGCTATGCC 2850

938 ArgThrSerIleArgAlaSerIleLeuThrPheAsnArgGlyProGlyLeuL
2851 CGGACCTCCATCAGAGCCTTCAACCGGGGTCCTGCGCTTCAACCGCGGGCCTGG 2900

955 YrArgAsnMetArgArgValLysPheValGluProLeuLysLysSerHisS
2901 GAGGAACATGCGTCGCGAAAACTCTTTGGGGTCTTGCCGGCTGAAGTGCACA 2950

972 erLeuPheLeuAspLeuGlnLeuAsnSerLeuGlnThrValCysThrAsn
2951 GCCTGTTTCTGGATTTGCAGTTGAACAGCCTCCAGACGGTGTGCACCAAC 3000

989 IleTyrLysIleLeuLeuGlnLeuAlaTyrArgPheHisIleAlaCysValIle
3001 ATCTACAAGATCCTCTGCGGCTGCAGGCCTACAGGTTCACGCACATGTGTCT 3050

1005 uGlnLeuProPheHisSerGlnHisValTrpLysAsnProThrPhePheLeuA
3051 GCAGCTCCCCATTCATCAGCAGCATGTTGGAAGAACCCCACAATTTTTTCCTGC 3100
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1022 rgValIleSerAspThrAlaSerLeuCysTyrSerIleLeuLysAlaLys 1038
3101 GCGGTCATCTCTGACACGGCCTCCCTGCTGCTACTCCAATCCTGAAAGCCAAG 3150
     |||||||||||||||||||||||||||||||||||||||||||||||||||

1039 AsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAlaGlyProLeuProSe 1055
3151 AACGGCAGGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGGCCCTCTGCCCTC 3200
     |||||||||||||||||||||||||||||||||||||||||||||||||

1055 rgGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeuThrA 1072
3201 CGAGGCCGTGCAGTGGCTGTGCCACCAAGCAATTCCTGCTCAACCTGACTC 3250
     ||||||||||||||||||||||||||||||||||||||||||||||||||

1072 rgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1088
3251 GACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACACGCCAG 3300
     ||||||||||||||||||||||||||||||||||||||||||||||||

1089 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAl 1105
3301 ACGCAGCTGAGTCGGAAGCTCCCGGGGACCACGCTGACTGCCCTGGAGGC 3350
     ||||||||||||||||||||||||||||||||||||||||||||||||

1105 aAlaAlaAsnProAlaLeuProSerAspPheLysThrIleLeuAsp 1120
3351 CGCAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC 3396
     ||||||||||||||||||||||||||||||||||||||||||||||
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